

SEQUENCE LISTING

<110> Helentjaris, Tim
Bates, Nic
Allen, Stephen M.

<120> Novel Invertase Inhibitors and Methods
of Use

<130> 035718/208677

<150> US 60/181,509
<151> 2000-02-10

<160> 54

<170> FastSEQ for Windows Version 4.0

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gcc tgc tcc acg tcc aac gct tcc gtc cta caa gac gcg tgc aag tcc	157
Ala Cys Ser Thr Ser Asn Ala Ser Val Leu Gln Asp Ala Cys Lys Ser	
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ttc gcc gct aag atc ccg gac acc ggc tac gcc tac tgc atc aag ttc	205
Phe Ala Ala Lys Ile Pro Asp Thr Gly Tyr Ala Tyr Cys Ile Lys Phe	
35 40 45	
ttc cag gcc gac agg gga agc gcc ggc gcg gac aag cgt ggc ctc gcc	253
Phe Gln Ala Asp Arg Gly Ser Ala Gly Ala Asp Lys Arg Gly Leu Ala	
50 55 60	
gcc atc gcc gtg agg atc atg ggg gca gcc aag agc acc gcc agt	301
Ala Ile Ala Val Arg Ile Met Gly Ala Ala Lys Ser Thr Ala Ser	
65 70 75	
cac atc gcc gcc ctg cggtcc gag aag gac aag gag cggtctggc	349
His Ile Ala Ala Leu Arg Ala Ser Glu Lys Asp Lys Glu Arg Leu Ala	
80 85 90	

tgc ctc agc gat tgc tcc gag gtg tac gcg cag gcc gtg gac cag acc Cys Leu Ser Asp Cys Ser Glu Val Tyr Ala Gln Ala Val Asp Gln Thr 95 100 105 110	397
ggc gtg gcg gcg aag ggc atc gcc tcg ggc acg ccc cgg ggc cgc gcg Gly Val Ala Ala Lys Gly Ile Ala Ser Gly Thr Pro Arg Gly Arg Ala 115 120 125	445
gac gcg gtg atg gcg ctc agc acg gtg gag gat gcc ccc ggc acc tgt Asp Ala Val Met Ala Leu Ser Thr Val Glu Asp Ala Pro Gly Thr Cys 130 135 140	493
gag cag ggg ttc cag gac ctg agc gtg cgt tcg ccg ctg gcc tcg gag Glu Gln Gly Phe Gln Asp Leu Ser Val Arg Ser Pro Leu Ala Ser Glu 145 150 155	541
gac gcc ggg ttc cgg aag gat gcg tcc atc gcg ctg tct gta acg gcc Asp Ala Gly Phe Arg Lys Asp Ala Ser Ile Ala Leu Ser Val Thr Ala 160 165 170	589
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Ala Asp Arg Gly Ser Ala Gly Ala Asp Lys Arg Gly Leu Ala Ala Ile 50 55 60	
Ala Val Arg Ile Met Gly Ala Ala Ala Lys Ser Thr Ala Ser His Ile 65 70 75 80	
Ala Ala Leu Arg Ala Ser Glu Lys Asp Lys Glu Arg Leu Ala Cys Leu 85 90 95	
Ser Asp Cys Ser Glu Val Tyr Ala Gln Ala Val Asp Gln Thr Gly Val 100 105 110	
Ala Ala Lys Gly Ile Ala Ser Gly Thr Pro Arg Gly Arg Ala Asp Ala 115 120 125	
Val Met Ala Leu Ser Thr Val Glu Asp Ala Pro Gly Thr Cys Glu Gln 130 135 140	
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170

175

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gccgcctgc	gggcctccga	gaaggacaag	gagccgctgg	cgtgcctcag	cgattgctcc	300
gaggtgtacg	cgcaggccgt	gjaccagacc	ggcgtggccgg	cgaaggccat	cgctcgccggc	360
acgccccggg	gcccgcggc	cgcggtgatg	gjcgtcagca	cggtggagga	tgccccggc	420
acctgtgagc	aggggttcca	gjactgtgagc	gtgcgttcgc	cgctggcctc	ggaggacgcc	480
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Ala Thr Thr Lys Arg Glu Lys Val Ile Leu Val Leu Leu Phe Ser Leu	
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acg atg ctc cct ctc agc acc ctc ggc acc cgc tcc ggc ccg gcg gcc	156
Thr Met Leu Pro Leu Ser Thr Leu Gly Thr Arg Ser Gly Pro Ala Ala	
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gtg cag cac cac ggc cac ggc acc acc aag cac ccc tcg cct cct	204
Val Gln His His Gly His Gly Thr Thr Lys His Pro Ser Pro Pro	
35 40 45	

tca cca gcc acg gcg ctg gta cgc agc acg tgt aac tcc acg gcg	252
Ser Pro Ala Thr Ala Ala Leu Val Arg Ser Thr Cys Asn Ser Thr Ala	
50 55 60 65	

tac tac gac gtg tgc gtg tcc gcg ctg ggc gcc gac ccg tcc agc gcc	300
Tyr Tyr Asp Val Cys Val Ser Ala Leu Gly Ala Asp Pro Ser Ser Ala	
70 75 80	

acc gcc gac gtc cgc ggg ctc tcg acc atc gcc gtg tcc gcg gcc	348
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Thr Ala Asp Val Arg Gly Leu Ser Thr Ile Ala Val Ser Ala Ala Ala			
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gcc aac gcc tcg ggc ggc gcc acg gcc gcg gctc gcc aac ggc			396
Ala Asn Ala Ser Gly Gly Ala Ala Thr Ala Ala Ala Leu Ala Asn Gly			
100	105	110	
acc ggc acc gcg tcg tcg tcc aac gcg cag gcg gcc cct gcc acg gcc			444
Thr Gly Thr Ala Ser Ser Asn Ala Gln Ala Ala Pro Ala Thr Ala			
115	120	125	
tcc gcc gcc gcg gctg ctc cgc acg tgc gca gcc aag tac ggc cag			492
Ser Ala Ala Ala Leu Leu Arg Thr Cys Ala Ala Lys Tyr Gly Gln			
130	135	140	145
gcc cgg gac gcg ctg gcc gcc ggg gac tcc atc gcg cag cag gac			540
Ala Arg Asp Ala Leu Ala Ala Gly Asp Ser Ile Ala Gln Gln Asp			
150	155	160	
tac gac gtg gcg tcc gtg cac gtg agc gcc gcc gag tac ccg cag			588
Tyr Asp Val Ala Ser Val His Val Ser Ala Ala Ala Glu Tyr Pro Gln			
165	170	175	
gtg tgt agg gtg ctg ttc cgg cgg cag aag ccc ggg cag tac ccc gcg			636
Val Cys Arg Val Leu Phe Arg Arg Gln Lys Pro Gly Gln Tyr Pro Ala			
180	185	190	
gag ctg gcg gcg agg gag gag acg ctc agg cag ctc tgc tcc gtc gcg			684
Glu Leu Ala Ala Arg Glu Glu Thr Leu Arg Gln Leu Cys Ser Val Ala			
195	200	205	
ctc gac atc atc ggg ctc gcc tcc acc aac acc aac taa taagctagca			733
Leu Asp Ile Ile Gly Leu Ala Ser Thr Asn Thr Asn *			
210	215	220	
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ttggtttaat tactgtacgt attatattaa tttagcaggc acatgcacgc agatgcata			853
ttaaattata aaaagttgg tgtgcctgcc caatcaccgt ttgaagaatt atttgagcag			913
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aactcgag			981
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Ala Val Gln His His Gly His Gly Gly Thr Thr Lys His Pro Ser Pro			
35	40	45	

Pro	Ser	Pro	Ala	Thr	Ala	Ala	Leu	Val	Arg	Ser	Thr	Cys	Asn	Ser	Thr
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Ala	Tyr	Tyr	Asp	Val	Cys	Val	Ser	Ala	Leu	Gly	Ala	Asp	Pro	Ser	Ser
65							70			75					80
Ala	Thr	Ala	Asp	Val	Arg	Gly	Leu	Ser	Thr	Ile	Ala	Val	Ser	Ala	Ala
							85			90					95
Ala	Ala	Asn	Ala	Ser	Gly	Gly	Ala	Ala	Thr	Ala	Ala	Ala	Leu	Ala	Asn
							100			105					110
Gly	Thr	Gly	Thr	Ala	Ser	Ser	Ser	Asn	Ala	Gln	Ala	Ala	Pro	Ala	Thr
							115			120					125
Ala	Ser	Ala	Ala	Ala	Ala	Leu	Leu	Arg	Thr	Cys	Ala	Ala	Lys	Tyr	Gly
							130			135					140
Gln	Ala	Arg	Asp	Ala	Leu	Ala	Ala	Ala	Gly	Asp	Ser	Ile	Ala	Gln	Gln
145							150			155					160
Asp	Tyr	Asp	Val	Ala	Ser	Val	His	Val	Ser	Ala	Ala	Ala	Glu	Tyr	Pro
							165			170					175
Gln	Val	Cys	Arg	Val	Leu	Phe	Arg	Arg	Gln	Lys	Pro	Gly	Gln	Tyr	Pro
							180			185					190
Ala	Glu	Leu	Ala	Ala	Arg	Glu	Glu	Thr	Leu	Arg	Gln	Leu	Cys	Ser	Val
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 ggcaccacca agcaccctc gcctccttca ccagccacgg cggcgctggt acgcagcagc 180
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 aacgcgcagg cggccctgc cacggccttc gcccggcgcc cgctgtccg cacgtgcgc 420
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 gtgtgttcc ggcggcagaa gcccggccag taccggcg gctggccgc gagggaggag 600
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 <222> (6)...(644)

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gca gct att gtt gct ctc ttc ttc tac ctc tca ctc aca aca cca			98
Ala Ala Ile Val Ala Leu Phe Phe Tyr Leu Ser Leu Thr Thr Pro			
20	25	30	
tgc tcg gcg gcc tca cca gag ccc cat ccc cct acc aat act aca caa			146
Cys Ser Ala Ala Ser Pro Glu Pro His Pro Pro Thr Asn Thr Thr Gln			
35	40	45	
ttc atc aga acc tca tgc gga gtg act atg tac cct aag cta tgc ttc			194
Phe Ile Arg Thr Ser Cys Gly Val Thr Met Tyr Pro Lys Leu Cys Phe			
50	55	60	
aaa acc ctc tcg gct tat gcc agc acc atc caa aca agc cat atg gag			242
Lys Thr Leu Ser Ala Tyr Ala Ser Thr Ile Gln Thr Ser His Met Glu			
65	70	75	
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Leu Ala Asn Ala Ala Leu Cys Val Ser Leu Lys Gly Ala Gln Ser Ser			
80	85	90	95
tca aac aag gta ctg aag tta tca aaa ggg cag ggg cta agc cgt aga			338
Ser Asn Lys Val Leu Lys Leu Ser Lys Gly Gln Gly Leu Ser Arg Arg			
100	105	110	
gaa gcc gca gcg ata acg gat tgc att gag aac atg cag gac tcg gtg			386
Glu Ala Ala Ile Thr Asp Cys Ile Glu Asn Met Gln Asp Ser Val			
115	120	125	
gat gag ctc caa caa tct ctg gtg gcg atg aag gac ctt caa ggg cct			434
Asp Glu Leu Gln Ser Leu Val Ala Met Lys Asp Leu Gln Gly Pro			
130	135	140	
gat ttt caa atg aaa atg agt gat ata gtg aca tgg gtg agt gca gct			482
Asp Phe Gln Met Lys Met Ser Asp Ile Val Thr Trp Val Ser Ala Ala			
145	150	155	
ctg aca gat gaa gac aca tgc atg gat gga ttc gca gag cat gcc atg			530
Leu Thr Asp Glu Asp Thr Cys Met Asp Gly Phe Ala Glu His Ala Met			
160	165	170	175
aaa ggg gac ctt aag agc act att agg agc aat att gtg agt gtt gct			578
Lys Gly Asp Leu Lys Ser Thr Ile Arg Ser Asn Ile Val Ser Val Ala			
180	185	190	
cag tta acc agc aat gct ttg gcc atc atc aac aag ttt cta tct att			626
Gln Leu Thr Ser Asn Ala Leu Ala Ile Ile Asn Lys Phe Leu Ser Ile			
195	200	205	
cag ggc aat caa ctc taa gttactgtgt cctatgtgtc tactactagt			674
Gln Gly Asn Gln Leu *			

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<212> PRT

<213> Vitis L

<400> 8

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Ser Ala Ala Ser Pro Glu Pro His Pro Pro Thr Asn Thr Thr Gln Phe	
35 40 45	
Ile Arg Thr Ser Cys Gly Val Thr Met Tyr Pro Lys Leu Cys Phe Lys	
50 55 60	
Thr Leu Ser Ala Tyr Ala Ser Thr Ile Gln Thr Ser His Met Glu Leu	
65 70 75 80	
Ala Asn Ala Ala Leu Cys Val Ser Leu Lys Gly Ala Gln Ser Ser Ser	
85 90 95	
Asn Lys Val Leu Lys Leu Ser Lys Gly Gln Gly Leu Ser Arg Arg Glu	
100 105 110	
Ala Ala Ala Ile Thr Asp Cys Ile Glu Asn Met Gln Asp Ser Val Asp	
115 120 125	
Glu Leu Gln Gln Ser Leu Val Ala Met Lys Asp Leu Gln Gly Pro Asp	
130 135 140	
Phe Gln Met Lys Met Ser Asp Ile Val Thr Trp Val Ser Ala Ala Leu	
145 150 155 160	
Thr Asp Glu Asp Thr Cys Met Asp Gly Phe Ala Glu His Ala Met Lys	
165 170 175	
Gly Asp Leu Lys Ser Thr Ile Arg Ser Asn Ile Val Ser Val Ala Gln	
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<213> Vitis l

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acagatgaag acacatgcacatggattc gcagagcatg ccatgaaagg ggacctaag	540
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1 5 10 15	
ctc ctc ttc cat tct tcg ctt tcc tgt caa ctc atc cat caa aca tgc	98
Leu Leu Phe His Ser Ser Leu Ser Cys Gln Leu Ile His Gln Thr Cys	
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aag aga att gca gac aat gat ccc aat gtg agc tac aat tta tgc gtc	146
Lys Arg Ile Ala Asp Asn Asp Pro Asn Val Ser Tyr Asn Leu Cys Val	
35 40 45	
atg agc ctt gaa tca aat ccc atg agt gca aat gcg agc ctt gaa gaa	194
Met Ser Leu Glu Ser Asn Pro Met Ser Ala Asn Ala Ser Leu Glu Glu	
50 55 60	
ctt gga gtc atc gca gtc gag cta gcc ttg tct aat gcg aca tac atc	242
Leu Gly Val Ile Ala Val Glu Leu Ala Leu Ser Asn Ala Thr Tyr Ile	
65 70 75	
aat tgg tac att agc aat aag ctt ttg cag gag aaa ggg ttt gat cca	290
Asn Trp Tyr Ile Ser Asn Lys Leu Leu Gln Glu Lys Gly Phe Asp Pro	
80 85 90 95	
ttt gcc gag gct tgc cta aaa gat tgt cat gaa ctt tac tcc gac gcc	338
Phe Ala Glu Ala Cys Leu Lys Asp Cys His Glu Leu Tyr Ser Asp Ala	
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atc cct gag tta aaa gat gtg ctc gat gat ttt aag gac aaa gac tac	386
Ile Pro Glu Leu Lys Asp Val Leu Asp Asp Phe Lys Asp Lys Asp Tyr	
115 120 125	
tac aag gct aat ata gag ttg agc gca gcc atg gag gcg tcg gct act	434
Tyr Lys Ala Asn Ile Glu Leu Ser Ala Ala Met Glu Ala Ser Ala Thr	
130 135 140	
tgt gaa gat ggt tac aag gaa agg aaa ggt gaa gtg tct ccc ttg gca	482
Cys Glu Asp Gly Tyr Lys Glu Arg Lys Gly Glu Val Ser Pro Leu Ala	

145

150

155

aaa gag gac aac aac ttc ttt caa ttg tgt gca att gct ctt gct ttc 530
 Lys Glu Asp Asn Asn Phe Phe Gln Leu Cys Ala Ile Ala Leu Ala Phe
 160 165 170 175

act aat atg ttg cat tga tccaaatatgt cattgcaaga aatatgaatc 578
 Thr Asn Met Leu His *
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tcacaatctt taacctatat atataaggtt tagattaaaa aaaaaaaaaa aaaaa 633

<210> 11

<211> 180

<212> PRT

<213> Vitis L

<400> 11

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Leu Phe His Ser Ser Leu Ser Cys Gln Leu Ile His Gln Thr Cys Lys 20 25 30

Arg Ile Ala Asp Asn Asp Pro Asn Val Ser Tyr Asn Leu Cys Val Met 35 40 45

Ser Leu Glu Ser Asn Pro Met Ser Ala Asn Ala Ser Leu Glu Glu Leu 50 55 60

Gly Val Ile Ala Val Glu Leu Ala Leu Ser Asn Ala Thr Tyr Ile Asn 65 70 75 80

Trp Tyr Ile Ser Asn Lys Leu Leu Gln Glu Lys Gly Phe Asp Pro Phe 85 90 95

Ala Glu Ala Cys Leu Lys Asp Cys His Glu Leu Tyr Ser Asp Ala Ile 100 105 110

Pro Glu Leu Lys Asp Val Leu Asp Asp Phe Lys Asp Tyr Tyr 115 120 125

Lys Ala Asn Ile Glu Leu Ser Ala Ala Met Glu Ala Ser Ala Thr Cys 130 135 140

Glu Asp Gly Tyr Lys Glu Arg Lys Gly Glu Val Ser Pro Leu Ala Lys 145 150 155 160

Glu Asp Asn Asn Phe Phe Gln Leu Cys Ala Ile Ala Leu Ala Phe Thr 165 170 175

Asn Met Leu His

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<212> DNA

<213> Vitis l

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 cttgaagaac ttggagtcat cgcaagtcgag ctagccttgt ctaatgcgac atacatcaat 240

tggcacat	gcaataagct	tttgcaggag	aaagggttg	atccattgc	cgaggcttg	300										
ctaaaagatt	gtcatgaact	ttactccgac	gccatccctg	agttaaaaga	tgtgctcgat	360										
gatttaagg	acaaagacta	ctacaaggct	aatatagagt	tgagcgcagc	catggaggcg	420										
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				Met	Gly	Phe	Ala	Gly	Leu							
				1						5						
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Leu	Phe	Leu	Phe	Leu	Leu	Met	Ser	Leu	Leu	Gln	Leu	Phe	His	Pro	Gln	
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ctt	gtt	ctt	gtg	agc	ggt	gac	tat	gat	ttg	atc	cag	aaa	act	tgt	aga	212
Leu	Val	Leu	Val	Ser	Gly	Asp	Tyr	Asp	Leu	Ile	Gln	Lys	Thr	Cys	Arg	
						25		30			35					
agc	acc	aaa	tac	tac	gac	ctt	tgc	atc	tca	tcc	ctc	aaa	tct	gat	ccc	260
Ser	Thr	Lys	Tyr	Tyr	Asp	Leu	Cys	Ile	Ser	Ser	Leu	Lys	Ser	Asp	Pro	
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aac	agc	ccc	aat	gcc	gac	acc	aag	gga	ttg	gcg	atg	att	atg	gtt	gga	308
Asn	Ser	Pro	Asn	Ala	Asp	Thr	Lys	Gly	Leu	Ala	Met	Ile	Met	Val	Gly	
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Ile	Gly	Glu	Ala	Asn	Ala	Thr	Ala	Ile	Ser	Ser	Tyr	Leu	Ser	Ser	Gln	
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ttg	gtc	ggc	tct	gct	aat	gat	tca	tca	atg	aag	aag	atc	ctt	aag	gaa	404
Leu	Val	Gly	Ser	Ala	Asn	Asp	Ser	Ser	Met	Lys	Lys	Ile	Leu	Lys	Glu	
						90		95			100					
tgc	gtc	aac	agg	tac	aac	tat	tct	agc	gat	gcg	ctc	caa	gct	tcg	ctc	452
Cys	Val	Asn	Arg	Tyr	Asn	Tyr	Ser	Ser	Asp	Ala	Ile	Gln	Ala	Ser	Leu	
						105		110			115					
caa	gct	ttg	acc	atg	gag	gct	tat	gac	tat	gct	tcg	cat	gtt	ata		500
Gln	Ala	Leu	Thr	Met	Glu	Ala	Tyr	Asp	Tyr	Ala	Tyr	Val	His	Val	Ile	
						120		125			130					

gca gcc gca gat tat ccc aat gcc tgc cgc aat tct ttt aaa agg tgc	548
Ala Ala Ala Asp Tyr Pro Asn Ala Cys Arg Asn Ser Phe Lys Arg Cys	
135 140 145 150	
cca aga ttg cct tat cca ccg gaa ctc ggg cta aga gaa gat gtt ttg	596
Pro Arg Leu Pro Tyr Pro Pro Glu Leu Gly Leu Arg Glu Asp Val Leu	
155 160 165	
aag cat ctg tgt gat gtg gtc ttg gga att att gat ctt ctt gat tgg	644
Lys His Leu Cys Asp Val Val Leu Gly Ile Ile Asp Leu Leu Asp Trp	
170 175 180	
taa tggtctcccc tttgcttcat tcttggtgtt taatcaacat attgcagact	697
*	
tccaaaaata ttcgttgtt ttctttgatc tttgtacaat gacttccacc ttgtctttga	757
agccaaacccg tgcttgtaa ctgtagcgtt tgataagctt aaagcttata taactttatt	817
tgtctgcaaa aaaaaaaaaa aaaaaaaaa	844
<210> 14	
<211> 182	
<212> PRT	
<213> Vitis L	
<400> 14	
Met Gly Phe Ala Gly Leu Leu Phe Leu Phe Leu Leu Met Ser Leu Leu	
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Gln Leu Phe His Pro Gln Leu Val Leu Val Ser Gly Asp Tyr Asp Leu	
20 25 30	
Ile Gln Lys Thr Cys Arg Ser Thr Lys Tyr Tyr Asp Leu Cys Ile Ser	
35 40 45	
Ser Leu Lys Ser Asp Pro Asn Ser Pro Asn Ala Asp Thr Lys Gly Leu	
50 55 60	
Ala Met Ile Met Val Gly Ile Gly Glu Ala Asn Ala Thr Ala Ile Ser	
65 70 75 80	
Ser Tyr Leu Ser Ser Gln Leu Val Gly Ser Ala Asn Asp Ser Ser Met	
85 90 95	
Lys Lys Ile Leu Lys Glu Cys Val Asn Arg Tyr Asn Tyr Ser Ser Asp	
100 105 110	
Ala Leu Gln Ala Ser Leu Gln Ala Leu Thr Met Glu Ala Tyr Asp Tyr	
115 120 125	
Ala Tyr Val His Val Ile Ala Ala Ala Asp Tyr Pro Asn Ala Cys Arg	
130 135 140	
Asn Ser Phe Lys Arg Cys Pro Arg Leu Pro Tyr Pro Pro Glu Leu Gly	
145 150 155 160	
Leu Arg Glu Asp Val Leu Lys His Leu Cys Asp Val Val Leu Gly Ile	
165 170 175	
Ile Asp Leu Leu Asp Trp	
180	
<210> 15	

<211> 549
<212> DNA
<213> Vitis 1

<400> 15
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ccccagcttgc ttcttgcgat cggactat gattgtatcc agaaaacttgc tagaagcacc 120
aaatactacg acctttgcac ctcatccctc aaatctgtatcc ccaacagcccc caatgccgac 180
accaaggat tggcgatgtatgggttggat attggagagg ctaatgcac tgccatttcc 240
tcttacttgc cttcccaatt ggtcggctct gctaattgtt catcaatgaa gaagatcctt 300
aaggaatgcg tcaacaggta caactattctt agcgatgcgc tccaagcttgc gctccaagct 360
ttgaccatgg aggcttatgtatgc ctatgcttac gtgcgttta tagcagccgc agattatccc 420
aatgcctgcc gcaattctt taaaaggtgc ccaagattgc cttatccacc ggaactcggg 480
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gattggtaa 549

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<212> DNA
<213> Vitis 1

<220>
<221> CDS
<222> (121) ... (669)

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atg agg ctt tcc tcc agt ttc ttt ctc ctc acc ctc gta ttc tta ttc 168
Met Arg Leu Ser Ser Ser Phe Phe Leu Leu Thr Leu Val Phe Leu Phe
1 5 10 15
ttc atc ttt ccc gca gca acc agt tgc acc aag ctc ata gat gag 216
Phe Ile Phe Pro Ala Ala Thr Ser Cys Cys Thr Lys Leu Ile Asp Glu
20 25 30
acc tgc aag aac tct tca cac aat gac agt aac ttc agt tac agg ttc 264
Thr Cys Lys Asn Ser Ser His Asn Asp Ser Asn Phe Ser Tyr Arg Phe
35 40 45
tgc aag act tcc ctc cag gca gct ccg gcc agc cgc tgc gcc agt ctc 312
Cys Lys Thr Ser Leu Gln Ala Ala Pro Ala Ser Arg Cys Ala Ser Leu
50 55 60
cg gga ctg ggg ttg atc gcc atc aga tta ttc cg gat aac gcc acc 360
Arg Gly Leu Gly Leu Ile Ala Ile Arg Leu Phe Arg Asp Asn Ala Thr
65 70 75 80
gac acc aga tgt ttc atc aga gaa ctg ctc gga aag aag ggg ttg gac 408
Asp Thr Arg Cys Phe Ile Arg Glu Leu Leu Gly Lys Lys Gly Leu Asp
85 90 95
aca tct gtg aag atg cgt ttg gaa gat tgt ttg gac atg tat tcg gat 456

Thr Ser Val Lys Met Arg Leu Glu Asp Cys Leu Asp Met Tyr Ser Asp			
100	105	110	
gga gtc gaa tcc cta aca cag gcc att aaa ggg tac agg gct ggg gag		504	
Gly Val Glu Ser Leu Thr Gln Ala Ile Lys Gly Tyr Arg Ala Gly Glu			
115	120	125	
tat ttc gat gct aat gtc caa gtt tcg ggt gct atg act tat gct agt		552	
Tyr Phe Asp Ala Asn Val Gln Val Ser Gly Ala Met Thr Tyr Ala Ser			
130	135	140	
act tgt gaa gat ggt ttc cag gag aag gaa ggt ttg gtt tcg ccg ttg		600	
Thr Cys Glu Asp Gly Phe Gln Glu Lys Glu Gly Leu Val Ser Pro Leu			
145	150	155	160
acg aag caa aac gac gat gct ttt cag ttg ggt gcg ctc tct ctt tcg		648	
Thr Lys Gln Asn Asp Asp Ala Phe Gln Leu Gly Ala Leu Ser Leu Ser			
165	170	175	
att atg aat aag cag aag tga ttcatggctg gctgattggc tggctttgtt		699	
Ile Met Asn Lys Gln Lys *			
180			
tttttttaat tctgaggcaa tgcttctctt tttctaaata attaataattt actttcacaa		759	
aaaaaaaaaaaa aaaaaaa		775	
<210> 17			
<211> 182			
<212> PRT			
<213> Vitis 1			
<400> 17			
Met Arg Leu Ser Ser Ser Phe Phe Leu Leu Thr Leu Val Phe Leu Phe			
1	5	10	15
Phe Ile Phe Pro Ala Ala Thr Ser Cys Cys Thr Lys Leu Ile Asp Glu			
20	25	30	
Thr Cys Lys Asn Ser Ser His Asn Asp Ser Asn Phe Ser Tyr Arg Phe			
35	40	45	
Cys Lys Thr Ser Leu Gln Ala Ala Pro Ala Ser Arg Cys Ala Ser Leu			
50	55	60	
Arg Gly Leu Gly Leu Ile Ala Ile Arg Leu Phe Arg Asp Asn Ala Thr			
65	70	75	80
Asp Thr Arg Cys Phe Ile Arg Glu Leu Leu Gly Lys Lys Gly Leu Asp			
85	90	95	
Thr Ser Val Lys Met Arg Leu Glu Asp Cys Leu Asp Met Tyr Ser Asp			
100	105	110	
Gly Val Glu Ser Leu Thr Gln Ala Ile Lys Gly Tyr Arg Ala Gly Glu			
115	120	125	
Tyr Phe Asp Ala Asn Val Gln Val Ser Gly Ala Met Thr Tyr Ala Ser			
130	135	140	
Thr Cys Glu Asp Gly Phe Gln Glu Lys Glu Gly Leu Val Ser Pro Leu			
145	150	155	160
Thr Lys Gln Asn Asp Asp Ala Phe Gln Leu Gly Ala Leu Ser Leu Ser			

165
Ile Met Asn Lys Gln Lys
180

170

175

<210> 18
<211> 549
<212> DNA
<213> Vitis l

<400> 18
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gcagcaacca gttgtgcac caagctata gatgagacct gcaagaactc ttcacacaat 120
gacagtaact tcagttacag gttctgcaag acttccctcc aggcagctcc ggccagccgc 180
tgcgccagtc tccggggact ggggttgatc gccatcagat tattccggga taacgccacc 240
gacaccagat gtttcatcag agaactgctc ggaaagaagg gggtggacac atctgtgaag 300
atgcgtttgg aagattgttt ggacatgtat tcggatggag tcgaatccct aacacaggcc 360
attaaagggt acaggcgtgg ggagtatttc gatgtaatg tccaagttc ggggtctatg 420
acttatgcta gtacttgtga agatggttc caggagaagg aaggtttggt ttcgcgttg 480
acgaagcaaa acgacgatgc tttcagttt ggtgcgtct ctcttcgtat tatgaataag 540
cagaagtga 549

<210> 19
<211> 686
<212> DNA
<213> Vitis L

<220>
<221> CDS
<222> (11) ... (547)

<400> 19
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1 5 10

tcc cct ctc ttc ttt ggc caa aca ctc aac ccc gta gag gca gga gac 97
Ser Pro Leu Phe Phe Gly Gln Thr Leu Asn Pro Val Glu Ala Gly Asp
15 20 25

aaa cta att gaa agt gca tgc cac act gct gag gta cca gta gta tgc 145
Lys Leu Ile Glu Ser Ala Cys His Thr Ala Glu Val Pro Val Val Cys
30 35 40 45

atg cag tgt gta aaa tct gac gag cgt tcg ggg aaa gcc gat gcg gta 193
Met Gln Cys Val Lys Ser Asp Glu Arg Ser Gly Lys Ala Asp Ala Val
50 55 60

ggg att gcc aac atc atc gtc gac tgt ttg atg agc cac tct agc tac 241
Gly Ile Ala Asn Ile Ile Val Asp Cys Leu Met Ser His Ser Ser Tyr
65 70 75

ttg gca agc aac atg tcg aat tta ggt tct aat cct gaa cac aat gcc 289
Leu Ala Ser Asn Met Ser Asn Leu Gly Ser Asn Pro Glu His Asn Ala

80	85	90	
aca aaa tca gcc tat gaa cat tgc ttc ctg cac tgt tct gat gca aag			337
Thr Lys Ser Ala Tyr Glu His Cys Phe Leu His Cys Ser Asp Ala Lys			
95	100	105	
aag gcg cta aat tca gca gct ttg gag cta aag aat ggc agc tat gat			385
Lys Ala Leu Asn Ser Ala Ala Leu Glu Leu Lys Asn Gly Ser Tyr Asp			
110	115	120	125
agc gct gaa ctg tcc ttg cgc gaa gca gcg cta tat caa ggc aca tgc			433
Ser Ala Glu Leu Ser Leu Arg Glu Ala Ala Leu Tyr Gln Gly Thr Cys			
130	135	140	
cga tac gag ttt gtg agt tca aat gag act tat gtg cca cct aat gtt			481
Arg Tyr Glu Phe Val Ser Ser Asn Glu Thr Tyr Val Pro Pro Asn Val			
145	150	155	
tac tat gat ctg aag gtc ttt gat ata ctt act gtg gct gcc ttt aga			529
Tyr Tyr Asp Leu Lys Val Phe Asp Ile Leu Thr Val Ala Ala Phe Arg			
160	165	170	
att ata gag aag ctt tga ttaagagttt tggagggttt tcacctaatt			577
Ile Ile Glu Lys Leu *			
175			
gctcatcatc catgaaaaat aaagttcat gttgactagt agacatgtaa catgaaatat			637
tgagacataa catacacctc cttatcatct aaaaaaaaaa aaaaaaaaaa			686
<210> 20			
<211> 178			
<212> PRT			
<213> Vitis L			
<400> 20			
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Phe Phe Gly Gln Thr Leu Asn Pro Val Glu Ala Gly Asp Lys Leu Ile			
20	25	30	
Glu Ser Ala Cys His Thr Ala Glu Val Pro Val Val Cys Met Gln Cys			
35	40	45	
Val Lys Ser Asp Glu Arg Ser Gly Lys Ala Asp Ala Val Gly Ile Ala			
50	55	60	
Asn Ile Ile Val Asp Cys Leu Met Ser His Ser Ser Tyr Leu Ala Ser			
65	70	75	80
Asn Met Ser Asn Leu Gly Ser Asn Pro Glu His Asn Ala Thr Lys Ser			
85	90	95	
Ala Tyr Glu His Cys Phe Leu His Cys Ser Asp Ala Lys Lys Ala Leu			
100	105	110	
Asn Ser Ala Ala Leu Glu Leu Lys Asn Gly Ser Tyr Asp Ser Ala Glu			
115	120	125	
Leu Ser Leu Arg Glu Ala Ala Leu Tyr Gln Gly Thr Cys Arg Tyr Glu			
130	135	140	

Phe Val Ser Ser Asn Glu Thr Tyr Val Pro Pro Asn Val Tyr Tyr Asp
 145 150 155 160
 Leu Lys Val Phe Asp Ile Leu Thr Val Ala Ala Phe Arg Ile Ile Glu
 165 170 175
 Lys Leu

<210> 21
 <211> 537
 <212> DNA
 <213> Vitis 1

<400> 21
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 gtaccaggtag tatgcatgca gtgtgtaaaa tctgacgagc gttcggggaa agccgatgcg 180
 gtagggattt ccaacatcat cgtcgactgt ttgatgagcc actctagcta cttggcaagc 240
 aacatgtcga atttaggttc taatcctgaa cacaatgcca caaaatcagc ctatgaacat 300
 tgttcctgc actgttctga tgcaaagaag ggcgctaaatt cagcagctt ggagctaaag 360
 aatggcagct atgatagcgc tgaactgtcc ttgcgcgaag cagcgctata tcaaggcaca 420
 tgccgatacg agtttgcgat ttcaaatgag acttatgtgc cacctaatgt ttactatgat 480
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<210> 22
 <211> 709
 <212> DNA
 <213> Vitis 1

<220>
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 <222> (13) ... (558)

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 Met Ala Ser Leu Ser Gly Val Leu Leu Val His Ile
 1 5 10

tcc ctc atg gcc acc act ctc ttc tac tat cct tca cat gcg atc gga 99
 Ser Leu Met Ala Thr Thr Leu Phe Tyr Tyr Pro Ser His Ala Ile Gly
 15 20 25

caa gac gtc gtc gag cag gta tgc cag caa acg gag gac tat caa ttc 147
 Gln Asp Val Val Glu Gln Val Cys Gln Gln Thr Glu Asp Tyr Gln Phe
 30 35 40 45

tgt ttc aat acc atc ctc aga gat cct cgg act ccg gca gtt aac atg 195
 Cys Phe Asn Thr Ile Leu Arg Asp Pro Arg Thr Pro Ala Val Asn Met
 50 55 60

gag ggg ctg tgc ctc agt gtg gca ata acc ata gac cac gtt agg 243
 Glu Gly Leu Cys Leu Leu Ser Val Ala Ile Thr Ile Asp His Val Arg
 65 70 75

gaa gcg gtg gat aaa ata ccg ggg ctg ctg gag aaa gct act gat cca Glu Ala Val Asp Lys Ile Pro Gly Leu Leu Glu Lys Ala Thr Asp Pro	291
80 85 90	
gtg gac aag caa aga atg acg act tgc caa tcc aac tat gga gca gcg Val Asp Lys Gln Arg Met Thr Thr Cys Gln Ser Asn Tyr Gly Ala Ala	339
95 100 105	
gcg ggg gac ttc cag agg gcg tgg ggc tcg gct tct tca aag gct ttc Ala Gly Asp Phe Gln Arg Ala Trp Gly Ser Ala Ser Ser Lys Ala Phe	387
110 115 120 125	
cat gat gtg ctg ggc tgg gtt cag aag gga agt ggt cag gtt ata aac His Asp Val Leu Gly Trp Val Gln Lys Gly Ser Gly Gln Val Ile Asn	435
130 135 140	
tgt gaa aat ata tac cgg caa agt ccg ccg atc cgt gaa tct ccc ctc Cys Glu Asn Ile Tyr Arg Gln Ser Pro Pro Ile Arg Glu Ser Pro Leu	483
145 150 155	
aca gtt gac aac cac aac gtg att aaa tta gca gga att act ttg gtt Thr Val Asp Asn His Asn Val Ile Lys Leu Ala Gly Ile Thr Leu Val	531
160 165 170	
gtt ctt ggt atg ctt ggt gtt cgt tga agatggtgtg tcttccttga Val Leu Gly Met Leu Gly Val Arg *	578
175 180	
ggtaaagctc acgttcttgg aattaacgta caataaatgt ggaatgcaat actgttggtt ggtcaataaa aactgatgtg aatttactac tcaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaa a	638 698 709
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<211> 181	
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<213> Vitis 1	
<400> 23	
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Val Glu Gln Val Cys Gln Gln Thr Glu Asp Tyr Gln Phe Cys Phe Asn 35 40 45	
Thr Ile Leu Arg Asp Pro Arg Thr Pro Ala Val Asn Met Glu Gly Leu 50 55 60	
Cys Leu Leu Ser Val Ala Ile Thr Ile Asp His Val Arg Glu Ala Val 65 70 75 80	
Asp Lys Ile Pro Gly Leu Leu Glu Lys Ala Thr Asp Pro Val Asp Lys 85 90 95	
Gln Arg Met Thr Thr Cys Gln Ser Asn Tyr Gly Ala Ala Gly Asp 100 105 110	
Phe Gln Arg Ala Trp Gly Ser Ala Ser Ser Lys Ala Phe His Asp Val	

115	120	125													
Leu	Gly	Trp	Val	Gln	Lys	Gly	Ser	Gly	Gln	Val	Ile	Asn	Cys	Glu	Asn
130				135						140					
Ile	Tyr	Arg	Gln	Ser	Pro	Pro	Ile	Arg	Glu	Ser	Pro	Leu	Thr	Val	Asp
145				150					155			160			
Asn	His	Asn	Val	Ile	Lys	Leu	Ala	Gly	Ile	Thr	Leu	Val	Val	Leu	Gly
			165					170			175				
Met	Leu	Gly	Val	Arg											
			180												

<210> 24

<211> 546

<212> DNA

<213> Vitis l

<400> 24

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gaggactatc	aattctgttt	caataccatc	ctcagagatc	ctcggactcc	ggcagttaac	180
atggaggggc	tgtgcctcct	cagtgtggca	ataaccatag	accacgttag	ggaagcggtg	240
gataaaatac	cggggctgct	ggagaaagct	actgatccag	tggacaagca	aagaatgacg	300
acttgccaat	ccaaactatgg	agcagcggcg	ggggacttcc	agagggcgtg	gggctcggct	360
tcttcaaagg	ctttccatga	tgtgtggc	tgggttcaga	aggaaagtgg	tcaggttata	420
aactgtgaaa	atataaccg	gcaaagtccg	ccgatccgtg	aatctccct	cacagttgac	480
aaccacaacg	tgattaaatt	agcaggaatt	actttggttg	ttcttggtat	gcttgggttt	540
						546

<210> 25

<211> 1067

<212> DNA

<213> Zea mays

<220>

<221> CDS

<222> (68) ... (691)

<400> 25

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Met	Pro	Thr	Leu	Ile	Ile	Lys	Gly	Arg	Pro	Asn	Met	Ala
1			5			10						

tcc	gga	acg	ccc	tac	act	gcc	gtc	ggc	gtc	atc	ttc	ctc	tcc	gtc	ttc	157
Ser	Gly	Thr	Pro	Tyr	Thr	Ala	Val	Gly	Val	Ile	Phe	Leu	Ser	Val	Phe	
15				20				25				30				

ctc	gtc	gcc	gca	tcc	gca	ggc	cgc	acc	gct	gca	cct	gct	gcc	gct	205
Leu	Val	Ala	Ala	Ala	Ser	Ala	Gly	Arg	Thr	Ala	Ala	Pro	Ala	Ala	
				35				40			45				

ccg	tcg	agc	aag	tac	tcg	ctc	gag	gaa	gct	gag	cag	acc	gct	ggg	253
Pro	Ser	Ser	Lys	Tyr	Ser	Leu	Glu	Glu	Ala	Cys	Glu	Gln	Thr	Ala	Gly
				50			55			60					

cac gag gac ctg tgc gtg gag acg ctg tcc gcg gac ccg tcg tcc aag	301
His Glu Asp Leu Cys Val Glu Thr Leu Ser Ala Asp Pro Ser Ser Lys	
65 70 75	
act gcc gac act acg ggg ctc gca cggttg gcc atc cag gcg gca cag	349
Thr Ala Asp Thr Thr Gly Leu Ala Arg Leu Ala Ile Gln Ala Ala Gln	
80 85 90	
cggttgcg aac gcg tcg gag acg gcg acc tac ctc tcc agc atc tac gac gac	397
Arg Asn Ala Ser Glu Thr Ala Thr Tyr Leu Ser Ser Ile Tyr Asp Asp	
95 100 105 110	
gac agc ctt gag aac aag acg gcg cag ctg cag cag tgc ctt gaa aac	445
Asp Ser Leu Glu Asn Lys Thr Ala Gln Leu Gln Gln Cys Leu Glu Asn	
115 120 125	
tgc ggc gag agg tac gag tcg gcg gtg gag cag ctg tcg gac gcg acg	493
Cys Gly Glu Arg Tyr Glu Ser Ala Val Glu Gln Leu Ser Asp Ala Thr	
130 135 140	
tcg gcg ctg gac acg ggc gcg tac agc gag tcg gag gag ctg gtg gtg	541
Ser Ala Leu Asp Thr Gly Ala Tyr Ser Glu Glu Leu Val Val	
145 150 155	
gcg agc cag gct gag gtg agg ctg tgt cag cgt ggc tgc caa gcc gtg	589
Ala Ser Gln Ala Glu Val Arg Leu Cys Gln Arg Gly Cys Gln Ala Val	
160 165 170	
ccg aac cac cgc aac atc ctc tcg gcg cgc aac cgc aac gtc gac cag	637
Pro Asn His Arg Asn Ile Leu Ser Ala Arg Asn Arg Asn Val Asp Gln	
175 180 185 190	
ctc tgc agc atc gcg ctc gcc atc acc aag ctc atc cac gga ccg cca	685
Leu Cys Ser Ile Ala Leu Ala Ile Thr Lys Leu Ile His Gly Pro Pro	
195 200 205	
tct tga tacacaggac gtagtaaaca ttttagggctt gttcatttcg ccgttaatcc	741
Ser *	
atgtggattt ggtggattt agtcggttt attccatagc aagtcaaaat acatccaaat	801
ccatccaaat acacaccaat acacatggaa ttgaaggtgg ttccataactt gtaacgtaat	861
tggtaactaa tgatgacgtt aatcatatt tgtttaagtt taattataat cagataccac	921
ataaaaaaatt aatatcagac tatttaaatt tattaccgct ggtattcaag tgtgaatcat	981
gtggctatat caacttctat tgtaaggcaga ttgagagtag tcgggtggta accatattaa	1041
ataaaaaaaaaaaaaaa aaaaaaaaaa aaaaaaa	1067
<210> 26	
<211> 207	
<212> PRT	
<213> Zea mays	

<400> 26

Met Pro Thr Leu Ile Ile Ile Lys Gly Arg Pro Asn Met Ala Ser Gly
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Thr Pro Tyr Thr Ala Val Gly Val Ile Phe Leu Ser Val Phe Leu Val
20 25 30
Ala Ala Ala Ser Ala Gly Arg Thr Ala Ala Pro Ala Ala Ala Pro Ser
35 40 45
Ser Lys Tyr Ser Leu Glu Glu Ala Cys Glu Gln Thr Ala Gly His Glu
50 55 60
Asp Leu Cys Val Glu Thr Leu Ser Ala Asp Pro Ser Ser Lys Thr Ala
65 70 75 80
Asp Thr Thr Gly Leu Ala Arg Leu Ala Ile Gln Ala Ala Gln Arg Asn
85 90 95
Ala Ser Glu Thr Ala Thr Tyr Leu Ser Ser Ile Tyr Asp Asp Asp Ser
100 105 110
Leu Glu Asn Lys Thr Ala Gln Leu Gln Gln Cys Leu Glu Asn Cys Gly
115 120 125
Glu Arg Tyr Glu Ser Ala Val Glu Gln Leu Ser Asp Ala Thr Ser Ala
130 135 140
Leu Asp Thr Gly Ala Tyr Ser Glu Ser Glu Glu Leu Val Val Ala Ser
145 150 155 160
Gln Ala Glu Val Arg Leu Cys Gln Arg Gly Cys Gln Ala Val Pro Asn
165 170 175
His Arg Asn Ile Leu Ser Ala Arg Asn Arg Asn Val Asp Gln Leu Cys
180 185 190
Ser Ile Ala Leu Ala Ile Thr Lys Leu Ile His Gly Pro Pro Ser
195 200 205

<210> 27

<211> 624

<212> DNA

<213> Zea mays

<400> 27

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gcggcacctg cggcccgccgtc gtcgagcaag tactcgctcg aggaagcgtg cgagcagacc 180
gcggggcaccg aggacctgtg cgtggagacg ctgtccgcgg acccgtcgcc caagactgccc 240
gacactacgg ggctcgacag gttggccatc caggcggcac agcggAACgc gtccggagacg 300
gcatccatcacc tctccagcat ctacgacgac gacagccttg agaacaagac ggccgagctg 360
cagcagtgcctt ttgaaaactg cggcgagagg tacgagtcgg cggtgagca gctgtccggac 420
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 gaggctttagt actatgctta catgcacatc actgccgcca aagattaccc aaatgcttgc 420
 cacaacgctt tcaaacggta ccccggttg gcttacccctc gtatcttc tagtagagaa 480
 gatggtttga agcatatatg tggatgtggca atggggattt tagataatct tgattggtag 540

<210> 34
 <211> 814
 <212> DNA
 <213> Glycine max

<220>
 <221> CDS
 <222> (99) ... (638)

<400> 34
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 aaaatctaaa gacacaaaac accctcctat actctata atg gtt tct tct aag atc 116
 Met Val Ser Ser Lys Ile
 1 5

ttc ttc ctt ttt ctc ctc ttt cta gca cac ctt cat caa cat gca tct 164
 Phe Phe Leu Phe Leu Leu Phe Leu Ala His Leu His Gln His Ala Ser
 10 15 20

gtg gaa gga gat tcc agt ttg ata aag aga act tgc aag aac acc aag 212
 Val Glu Gly Asp Ser Ser Leu Ile Lys Arg Thr Cys Lys Asn Thr Lys
 25 30 35

tac tac aat cta tgc ttc tct tcc ctc aaa tct gat cca agc agt cca 260
 Tyr Tyr Asn Leu Cys Phe Ser Ser Leu Lys Ser Asp Pro Ser Ser Pro
 40 45 50

aac gca gat cct aag ggc cta gct gtg atc atg att gga ata gga atg Asn Ala Asp Pro Lys Gly Leu Ala Val Ile Met Ile Gly Ile Gly Met 55 60 65 70	308
acc aat gcc act tcc aca tcc tcc tac ttg tct tca aag ttg cct acc Thr Asn Ala Thr Ser Thr Ser Ser Tyr Leu Ser Ser Lys Leu Pro Thr 75 80 85	356
ccc tcc aac aac aca acc tgg aaa agg gtc ctc aag gag tgt gct gat Pro Ser Asn Asn Thr Thr Trp Lys Arg Val Leu Lys Glu Cys Ala Asp 90 95 100	404
aag tac tcc tat gct ggt gat gcc ctc caa gat tcg gtg cag gat ttg Lys Tyr Ser Tyr Ala Gly Asp Ala Leu Gln Asp Ser Val Gln Asp Leu 105 110 115	452
gct aat gag gct tat gac tat gct tac atg cac atc act gcc gcc aaa Ala Asn Glu Ala Tyr Asp Tyr Ala Tyr Met His Ile Thr Ala Ala Lys 120 125 130	500
gat tac cca aat gct tgc cac aac gct ttc aaa cgg tac cct ggt ttg Asp Tyr Pro Asn Ala Cys His Asn Ala Phe Lys Arg Tyr Pro Gly Leu 135 140 145 150	548
gtt tat cct cgt gat ctt gct cgt aga gaa gat ggt ttg aag cat ata Val Tyr Pro Arg Asp Leu Ala Arg Arg Glu Asp Gly Leu Lys His Ile 155 160 165	596
tgc gat gtg gca atg ggg att ata gat aat ctt gat tgg tag Cys Asp Val Ala Met Gly Ile Ile Asp Asn Leu Asp Trp * 170 175	638
gtgcatgcat ttgagtatat agcttccagt ttgttatgca aaccatgtta tatctctgg gttatgtttg gctaccttgt atcttgttaa ttatgttctt ggtataatat attggacata aatgttttag tctttttagaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 698 758 814	
<210> 35	
<211> 179	
<212> PRT	
<213> Glycine max	
<400> 35	
Met Val Ser Ser Lys Ile Phe Phe Leu Phe Leu Phe Leu Ala His 1 5 10 15	
Leu His Gln His Ala Ser Val Glu Gly Asp Ser Ser Leu Ile Lys Arg 20 25 30	
Thr Cys Lys Asn Thr Lys Tyr Tyr Asn Leu Cys Phe Ser Ser Leu Lys 35 40 45	
Ser Asp Pro Ser Ser Pro Asn Ala Asp Pro Lys Gly Leu Ala Val Ile 50 55 60	
Met Ile Gly Ile Gly Met Thr Asn Ala Thr Ser Thr Ser Ser Tyr Leu 65 70 75 80	

<210> 36
<211> 540
<212> DNA
<213> Glycine max

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<400> 36
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gcatctgtgg aaggagattc cagtttgata aagagaacct gcaagaacac caagtactac 120
aatctatgct tctcttccct caaatctgat ccaaggcgtc caaacgcaga tcctaaggc 180
ctagctgtga tcatgattgg aataggaatg accaatgcc  cttccacatc ctcctacttg 240
tcttcaaagt tgccctacccc ctccaaacaac acaacctgga aaagggtcct caaggagtgt 300
gctgataagt actcctatgc tggtgatgcc ctccaaagatt cggtgccagg  tttggctaat 360
gaggctttag actatgctt catgcacatc actgccgcc  aagattaccc aaatgcttgc 420
cacaacgctt tcaaacggta ccctggttt gtttatcctc gtgatcttgc tcgttagagaa 480
gatggtttga agatatatatg cgtatgtggca atggggattt tagataatct tgattggtag 540
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<210> 37
<211> 766
<212> DNA
<213> Glycine max

<220>
<221> CDS
<222> (6) ... (542)

<400> 37
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Met Thr Asn Leu Lys Pro Leu Ile Leu Leu Ala Ile Ile Val Met
1 5 10 15

att tca ata cca tca agc cac tgc aga acc ttg ctt cca gaa aat gaa 98
 Ile Ser Ile Pro Ser Ser His Cys Arg Thr Leu Leu Pro Glu Asn Glu
 20 25 30

aag ctg ata gag aac act tgc agg aag acc ccc aac tac aac gtt tgc 146
 Lys Leu Ile Glu Asn Thr Cys Arg Lys Thr Pro Asn Tyr Asn Val Cys
 35 40 45

ctt gag tct ctg aag gca agc cct ggg agc tcc agt gct gac gtc aca Leu Glu Ser Leu Lys Ala Ser Pro Gly Ser Ser Ser Ala Asp Val Thr 50 55 60	194
ggg cta gct caa atc atg gtg aaa gag atg aag gca aaa gca aac tat Gly Leu Ala Gln Ile Met Val Lys Glu Met Lys Ala Lys Ala Asn Tyr 65 70 75	242
gca ttg aag aga atc cag gag ctg cag agg gtg gga gca ggg cct aat Ala Leu Lys Arg Ile Gln Glu Leu Gln Arg Val Gly Ala Gly Pro Asn 80 85 90 95	290
aag caa aga aga gcc ttg agt tct tgt gtt gat aaa tac aaa acg gtt Lys Gln Arg Arg Ala Leu Ser Ser Cys Val Asp Lys Tyr Lys Thr Val 100 105 110	338
tta att gct gat gtt cca caa gcc act gag gct ctg cag aaa ggg gac Leu Ile Ala Asp Val Pro Gln Ala Thr Glu Ala Leu Gln Lys Gly Asp 115 120 125	386
ccc aag ttt gct gaa gat ggg gct aat gat gct gct aat gag gct acc Pro Lys Phe Ala Glu Asp Gly Ala Asn Asp Ala Ala Asn Glu Ala Thr 130 135 140	434
ttt tgt gag gct gat ttc tct gct ggg aat tcc cca ctc acc aaa cag Phe Cys Glu Ala Asp Phe Ser Ala Gly Asn Ser Pro Leu Thr Lys Gln 145 150 155	482
aac aat gct atg cat gat gtt gct gct gtt act gcc gct att gtt aga Asn Asn Ala Met His Asp Val Ala Ala Val Thr Ala Ala Ile Val Arg 160 165 170 175	530
ttg ttg ctc taa taattctagt tgctgaaacc tatatatatg ctttaattgtta Leu Leu Leu *	582
ttaactaaat atagattata gatgtctctg catcatgctg acttgggcc tggtaactgt aatgtgaaaa tactatcttt ttataaaaat gttttatataat gtaataaaaat ccaaccctct cgtgattctc acgagttcc cagaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa aaaa	642 702 762 766
<210> 38 <211> 178 <212> PRT <213> Glycine max	
<400> 38 Met Thr Asn Leu Lys Pro Leu Ile Leu Ala Ile Ile Val Met Ile 1 5 10 15 Ser Ile Pro Ser Ser His Cys Arg Thr Leu Leu Pro Glu Asn Glu Lys 20 25 30 Leu Ile Glu Asn Thr Cys Arg Lys Thr Pro Asn Tyr Asn Val Cys Leu 35 40 45	

Glu Ser Leu Lys Ala Ser Pro Gly Ser Ser Ser Ala Asp Val Thr Gly
 50 55 60
 Leu Ala Gln Ile Met Val Lys Glu Met Lys Ala Lys Ala Asn Tyr Ala
 65 70 75 80
 Leu Lys Arg Ile Gln Glu Leu Gln Arg Val Gly Ala Gly Pro Asn Lys
 85 90 95
 Gln Arg Arg Ala Leu Ser Ser Cys Val Asp Lys Tyr Lys Thr Val Leu
 100 105 110
 Ile Ala Asp Val Pro Gln Ala Thr Glu Ala Leu Gln Lys Gly Asp Pro
 115 120 125
 Lys Phe Ala Glu Asp Gly Ala Asn Asp Ala Ala Asn Glu Ala Thr Phe
 130 135 140
 Cys Glu Ala Asp Phe Ser Ala Gly Asn Ser Pro Leu Thr Lys Gln Asn
 145 150 155 160
 Asn Ala Met His Asp Val Ala Ala Val Thr Ala Ala Ile Val Arg Leu
 165 170 175
 Leu Leu

<210> 39

<211> 537

<212> DNA

<213> Glycine max

<400> 39

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agccactgca gaaccttgc tccagaaaaat gaaaagctga tagagaacac ttgcaggaag	120
acccccaact acaacgtttg ccttgagctt ctgaaggcaa gccctgggag ctccagtgc	180
gacgtcacag ggctagctca aatcatggtg aaagagatga aggcaaaagc aaactatgc	240
ttgaagagaa tccaggagct gcagaggggtg ggagcagggc ctaataagca aagaagagcc	300
tttagttctt gtgttataa atacaaaacg gtttaattt ctgtatgtcc acaagccact	360
gaggctctgc agaaagggaa ccccaagtt gctgaagatg gggctaattga tgctgctaatt	420
gaggctaccc tttgtgaggc tgatttctt gctggattt ccccaactcac caaacagaac	480
aatgctatgc atgatgttgc tgctgttact gcccgtattt ttagattttt gctctaa	537

<210> 40

<211> 826

<212> DNA

<213> Glycine max

<220>

<221> CDS

<222> (111)...(719)

<221> misc_feature

<222> (1)...(826)

<223> n = A,T,C or G

<400> 40

aaaaggttag gtccactaca tctgctccta accataaaaa ggcctagcag cattccattc	60
agtggatct agcaactacc aaaaccaatc tcttcaata atcaacaaca atg aca	116
Met Thr	
1	

aac ttg aag cct cta att ctc ttc ttt tat ctc cta gcc att gtt gtt		164	
Asn Leu Lys Pro Leu Ile Leu Phe Phe Tyr Leu Leu Ala Ile Val Val			
5	10	15	
atg att tca ata cca tca agc cac tgc agc aga acc ttg ctt cca gaa		212	
Met Ile Ser Ile Pro Ser Ser His Cys Ser Arg Thr Leu Leu Pro Glu			
20	25	30	
aac gaa aag ctg ata gag aac act tgc aag aaa act ccc aac tac aac		260	
Asn Glu Lys Leu Ile Glu Asn Thr Cys Lys Lys Thr Pro Asn Tyr Asn			
35	40	45	50
gtt tgc ctt gag tct ctg aag gca agc cct ggg agc tcc agt gct gac		308	
Val Cys Leu Glu Ser Leu Lys Ala Ser Pro Gly Ser Ser Ala Asp			
55	60	65	
gtc aca ggg ctg gct caa atc atg gtc aaa gag atg aag gcc aaa gca		356	
Val Thr Gly Leu Ala Gln Ile Met Val Lys Glu Met Lys Ala Lys Ala			
70	75	80	
aac gat gca ttg aaa aga atc caa gag ttg cag agg gtg gga gca tcg		404	
Asn Asp Ala Leu Lys Arg Ile Gln Glu Leu Gln Arg Val Gly Ala Ser			
85	90	95	
ggg cct aag caa aga aga gcc ttg agt tct tgt gct gat aaa tac aaa		452	
Gly Pro Lys Gln Arg Arg Ala Leu Ser Ser Cys Ala Asp Lys Tyr Lys			
100	105	110	
gcg gtt tta att gct gat gtt cca caa gcc act gag gct ctg cag aaa		500	
Ala Val Leu Ile Ala Asp Val Pro Gln Ala Thr Glu Ala Leu Gln Lys			
115	120	125	130
ggt gac ccc aag ttt gct gaa gat ggg gct aat gat gct gct aat gag		548	
Gly Asp Pro Lys Phe Ala Glu Asp Gly Ala Asn Asp Ala Ala Asn Glu			
135	140	145	
gct act tat tgt gag act gat ttc tct gca gca ggg aat tcc cca ctc		596	
Ala Thr Tyr Cys Glu Thr Asp Phe Ser Ala Ala Gly Asn Ser Pro Leu			
150	155	160	
acc aaa cag aac aat gct atg cat gat gtt gct gct act gcc gct		644	
Thr Lys Gln Asn Asn Ala Met His Asp Val Ala Ala Val Thr Ala Ala			
165	170	175	
att gtt aaa ttg ttg ctc caa act ata tat act aaa ttg tac ctg tta		692	
Ile Val Lys Leu Leu Gln Thr Ile Tyr Thr Lys Leu Tyr Leu Leu			
180	185	190	
act gta atg gtg aaa ata cta tcc taa tttaaaaagc cttttttata		739	
Thr Val Met Val Lys Ile Leu Ser *			
195	200		

aaaatngttt attaatatgt taataaaaat ccaaaccctc cccgtngaat tctcaacaaa 799
tttcccaaaa aaaaaaaaaa aaaaaaaaa 826

<210> 41
<211> 202
<212> PRT
<213> Glycine max

<400> 41

Met	Thr	Asn	Leu	Lys	Pro	Leu	Ile	Leu	Phe	Phe	Tyr	Leu	Leu	Ala	Ile	
1					5				10						15	
Val	Val	Met	Ile	Ser	Ile	Pro	Ser	Ser	His	Cys	Ser	Arg	Thr	Leu	Leu	
					20				25						30	
Pro	Glu	Asn	Glu	Lys	Leu	Ile	Glu	Asn	Thr	Cys	Lys	Lys	Thr	Pro	Asn	
					35				40						45	
Tyr	Asn	Val	Cys	Leu	Glu	Ser	Leu	Lys	Ala	Ser	Pro	Gly	Ser	Ser	Ser	
					50				55						60	
Ala	Asp	Val	Thr	Gly	Leu	Ala	Gln	Ile	Met	Val	Lys	Glu	Met	Lys	Ala	
					65				70			75			80	
Lys	Ala	Asn	Asp	Ala	Leu	Lys	Arg	Ile	Gln	Glu	Leu	Gln	Arg	Val	Gly	
					85				90						95	
Ala	Ser	Gly	Pro	Lys	Gln	Arg	Arg	Ala	Leu	Ser	Ser	Cys	Ala	Asp	Lys	
					100				105						110	
Tyr	Lys	Ala	Val	Leu	Ile	Ala	Asp	Val	Pro	Gln	Ala	Thr	Glu	Ala	Leu	
					115				120						125	
Gln	Lys	Gly	Asp	Pro	Lys	Phe	Ala	Glu	Asp	Gly	Ala	Asn	Asp	Ala	Ala	
					130				135						140	
Asn	Glu	Ala	Thr	Tyr	Cys	Glu	Thr	Asp	Phe	Ser	Ala	Ala	Gly	Asn	Ser	
					145				150						160	
Pro	Leu	Thr	Lys	Gln	Asn	Asn	Ala	Met	His	Asp	Val	Ala	Ala	Val	Thr	
					165				170						175	
Ala	Ala	Ile	Val	Lys	Leu	Leu	Gln	Thr	Ile	Tyr	Thr	Lys	Leu	Tyr		
					180				185						190	
Leu	Leu	Thr	Val	Met	Val	Lys	Ile	Leu	Ser							
					195				200							

<210> 42
<211> 609
<212> DNA
<213> Glycine max

<400> 42

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aacacttgca	agaaaactcc	caactacaac	gttgccttg	agtctctgaa	ggcaagccct	180
gggagctcca	gtgctgacgt	cacagggctg	gctcaaatca	tggtaaaga	gatgaaggcc	240
aaagcaaacg	atgcattgaa	aagaatccaa	gagttgcaga	gggtgggagc	atcggggcct	300
aagcaaagaa	gagccttgag	ttcttgctg	gataaataca	aagcggttt	aattgctgat	360
gttccacaag	ccactgaggc	tctgcagaaa	ggtgacccca	agtttgctga	agatggggct	420
aatgatgctg	ctaatgaggc	tacttattgt	gagactgatt	tctctgcagc	agggaaattcc	480
ccactcacca	aacagaacaa	tgctatgcat	gatgttgctg	ctgttactgc	cgctattgtt	540
aaattgttgc	tccaaactat	atatactaaa	ttgtacctgt	taactgtaat	ggtgaaaata	600
ctatcctaa						609

<210> 43
<211> 983
<212> DNA
<213> Glycine max

<220>
<221> CDS
<222> (50) ... (598)

<400> 43
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Met Lys Ile
1

atg gaa tca tta gct ctt atc ttc tac agt act ctt gtt tta gct acg 106
Met Glu Ser Leu Ala Leu Ile Phe Tyr Ser Thr Leu Val Leu Ala Thr
5 10 15

att tca gtt cca gca act aac tcc aga atc atc cat caa aaa aac aat 154
Ile Ser Val Pro Ala Thr Asn Ser Arg Ile Ile His Gln Lys Asn Asn
20 25 30 35

gcc aat ctg att gaa gaa act tgc aag cag aca ccc cat cac gac ctt 202
Ala Asn Leu Ile Glu Glu Thr Cys Lys Gln Thr Pro His His Asp Leu
40 45 50

tgc atc caa tac ctc tcc tcc gac cct cgc agc acc gaa gca gat gtg 250
Cys Ile Gln Tyr Leu Ser Ser Asp Pro Arg Ser Thr Glu Ala Asp Val
55 60 65

aca ggg ctg gca ctt att atg gtc aac gta atc aaa atc aaa gca aac 298
Thr Gly Leu Ala Leu Ile Met Val Asn Val Ile Lys Ile Lys Ala Asn
70 75 80

aat gca ttg gac aaa atc cac caa ctg ctt cag aaa aac cct gaa cct 346
Asn Ala Leu Asp Lys Ile His Gln Leu Leu Gln Lys Asn Pro Glu Pro
85 90 95

agt caa aag gaa cca ctg agt tcg tgt gct gct aga tac aaa gca att 394
Ser Gln Lys Glu Pro Leu Ser Ser Cys Ala Ala Arg Tyr Lys Ala Ile
100 105 110 115

gtg gaa gct gac gtg gca caa gcc gtt gcg tct ctg cag aaa gga gac 442
Val Glu Ala Asp Val Ala Gln Ala Val Ala Ser Leu Gln Lys Gly Asp
120 125 130

ccc aag ttc gca gaa gat ggt gcc aat gat gct gct att gag gcc acc 490
Pro Lys Phe Ala Glu Asp Gly Ala Asn Asp Ala Ala Ile Glu Ala Thr
135 140 145

act tgt gag aac agc ttc tct gct ggg aaa tcg cca ctc acc aat cac 538
Thr Cys Glu Asn Ser Phe Ser Ala Gly Lys Ser Pro Leu Thr Asn His

150

155

160

aac aat gct atg cac gat gtt gca acc ata act gca gct ata gtt aga 586
 Asn Asn Ala Met His Asp Val Ala Thr Ile Thr Ala Ala Ile Val Arg
 165 170 175

caa ttg ctc tag tgacacttac tccaacggag gggatgatgc aatttaattt 638
 Gln Leu Leu *
 180

tcgtaatatac acattataat tatattttca attaacacaa cataaaatct tgctctttg 698
 ttggctctttt ctgtaatgga aacacaactg ctttgccac ttcacaattc tcatttctca 758
 ctgtcccttc tcctctgctt tccacgtttc ttatttcat ttttcttctt tgattcttgg 818
 aaaataattt acagcgcattt ggtatgtgata tgcctctgtc ttgtgcttctt actttcttctt 878
 aatgtatcat caatttagcc ttttaactt taacaaacat ttgttaatca gatccttcat 938
 attatgaaga tattgacatt taaaacttaaa aaaaaaaaaa aaaaa 983

<210> 44
 <211> 182
 <212> PRT
 <213> Glycine max

<400> 44
 Met Lys Ile Met Glu Ser Leu Ala Leu Ile Phe Tyr Ser Thr Leu Val
 1 5 10 15
 Leu Ala Thr Ile Ser Val Pro Ala Thr Asn Ser Arg Ile Ile His Gln
 20 25 30
 Lys Asn Asn Ala Asn Leu Ile Glu Glu Thr Cys Lys Gln Thr Pro His
 35 40 45
 His Asp Leu Cys Ile Gln Tyr Leu Ser Ser Asp Pro Arg Ser Thr Glu
 50 55 60
 Ala Asp Val Thr Gly Leu Ala Leu Ile Met Val Asn Val Ile Lys Ile
 65 70 75 80
 Lys Ala Asn Asn Ala Leu Asp Lys Ile His Gln Leu Leu Gln Lys Asn
 85 90 95
 Pro Glu Pro Ser Gln Lys Glu Pro Leu Ser Ser Cys Ala Ala Arg Tyr
 100 105 110
 Lys Ala Ile Val Glu Ala Asp Val Ala Gln Ala Val Ala Ser Leu Gln
 115 120 125
 Lys Gly Asp Pro Lys Phe Ala Glu Asp Gly Ala Asn Asp Ala Ala Ile
 130 135 140
 Glu Ala Thr Thr Cys Glu Asn Ser Phe Ser Ala Gly Lys Ser Pro Leu
 145 150 155 160
 Thr Asn His Asn Asn Ala Met His Asp Val Ala Thr Ile Thr Ala Ala
 165 170 175
 Ile Val Arg Gln Leu Leu
 180

<210> 45
 <211> 549
 <212> DNA
 <213> Glycine max

<400> 45

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 gaaacttgca agcagacacc ccatcacgac cttgcattcc aataccttc ctccgaccct 180
 cgcagcaccg aagcagatgt gacagggctg gcacttatta tggtaacgt aatcaaatac 240
 aaagcaaaca atgcattgga caaaatccac caactgcttc agaaaaaccc tgaacctagt 300
 caaaaggaac cactgagttc gtgtgctgct agatacaaag caattgtgga agctgacgtg 360
 gcacaagccg ttgcgtctct gcagaaagga gaccccaagt tcgcagaaga tggtgccaat 420
 gatgctgcta ttgaggccac cacttgtgag aacagcttct ctgctggaa atcgccactc 480
 accaatcaca acaatgctat gcacgatgtt gcaaccataa ctgcagctat agttagacaa 540
 ttgctctag 549

<210> 46

<211> 609

<212> DNA

<213> Glycine max

<220>

<221> CDS

<222> (16) ... (609)

<400> 46

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Met Met Leu Gln Ala Ser Phe Leu Arg Leu Ile Ser	
1 5 10	
ttc ttc ttt ctc atc gca ctc cct ctt gga aga agc tct acc acc ttg	99
Phe Phe Phe Leu Ile Ala Leu Pro Leu Gly Arg Ser Ser Thr Thr Leu	
15 20 25	
aat gta cca aag gac ata atc aac caa aca tgc caa aaa tgt gcc aac	147
Asn Val Pro Lys Asp Ile Ile Asn Gln Thr Cys Gln Lys Cys Ala Asn	
30 35 40	
caa tcc atc atc ttg agc tac aag cta tgc tcc act tct ctt ccg acg	195
Gln Ser Ile Ile Leu Ser Tyr Lys Leu Cys Ser Thr Ser Leu Pro Thr	
45 50 55 60	
gtt ccg gtg agt cac tcc gca aat ctc gaa ggg ttg gcg ttg gtt gca	243
Val Pro Val Ser His Ser Ala Asn Leu Glu Gly Leu Ala Leu Val Ala	
65 70 75	
atg gag cta gca cta gag aat gtc act agc act ttg gca atc ata gag	291
Met Glu Leu Ala Leu Glu Asn Val Thr Ser Thr Leu Ala Ile Ile Glu	
80 85 90	
aag cta tta gat agc aca agt ttg gat aat tct gct ttg ggg tgc tta	339
Lys Leu Leu Asp Ser Thr Ser Leu Asp Asn Ser Ala Leu Gly Cys Leu	
95 100 105	
gca gat tgc ttg gaa ctg tac tct gat gca gca tgg aca ata ctg aat	387
Ala Asp Cys Leu Glu Leu Tyr Ser Asp Ala Ala Trp Thr Ile Leu Asn	
110 115 120	

tcc gta ggt gtt ttc ttg tct ggg aat tat gat gta act agg att tgg	435
Ser Val Gly Val Phe Leu Ser Gly Asn Tyr Asp Val Thr Arg Ile Trp	
125 130 135 140	
atg agt tca gtt atg gaa gca gca tca aca tgc caa caa ggt ttt act	483
Met Ser Ser Val Met Glu Ala Ala Ser Thr Cys Gln Gln Gly Phe Thr	
145 150 155	
gag aga ggt gaa gct tct cct ttg aca cag gag aat tat aat ctc ttt	531
Glu Arg Gly Glu Ala Ser Pro Leu Thr Gln Glu Asn Tyr Asn Leu Phe	
160 165 170	
cag ttg tgt ggt att gca ctt tgc att att cat ttg gct aca cct gga	579
Gln Leu Cys Gly Ile Ala Leu Cys Ile Ile His Leu Ala Thr Pro Gly	
175 180 185	
gta cct tat tct caa tta ttc cac aga taa	609
Val Pro Tyr Ser Gln Leu Phe His Arg *	
190 195	
<210> 47	
<211> 197	
<212> PRT	
<213> Glycine max	
<400> 47	
Met Met Leu Gln Ala Ser Phe Leu Arg Leu Ile Ser Phe Phe Leu	
1 5 10 15	
Ile Ala Leu Pro Leu Gly Arg Ser Ser Thr Thr Leu Asn Val Pro Lys	
20 25 30	
Asp Ile Ile Asn Gln Thr Cys Gln Lys Cys Ala Asn Gln Ser Ile Ile	
35 40 45	
Leu Ser Tyr Lys Leu Cys Ser Thr Ser Leu Pro Thr Val Pro Val Ser	
50 55 60	
His Ser Ala Asn Leu Glu Gly Leu Ala Leu Val Ala Met Glu Leu Ala	
65 70 75 80	
Leu Glu Asn Val Thr Ser Thr Leu Ala Ile Ile Glu Lys Leu Leu Asp	
85 90 95	
Ser Thr Ser Leu Asp Asn Ser Ala Leu Gly Cys Leu Ala Asp Cys Leu	
100 105 110	
Glu Leu Tyr Ser Asp Ala Ala Trp Thr Ile Leu Asn Ser Val Gly Val	
115 120 125	
Phe Leu Ser Gly Asn Tyr Asp Val Thr Arg Ile Trp Met Ser Ser Val	
130 135 140	
Met Glu Ala Ala Ser Thr Cys Gln Gln Gly Phe Thr Glu Arg Gly Glu	
145 150 155 160	
Ala Ser Pro Leu Thr Gln Glu Asn Tyr Asn Leu Phe Gln Leu Cys Gly	
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aaatgtgcca accaatccat catcttgagc tacaagctat gctccacttc tcttccgacg 180
gttccggtga gtcactccgc aaatctcgaa gggttggcgt tggttgcaat ggagctagca 240
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Ser Leu Leu Val Val Val Leu Leu Leu Val Ser Ser Ser Ala Ser Ile
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cta gaa gat acc tgc aag cgc ttc gac ggc gct gac atc tat gat atc 149
 Leu Glu Asp Thr Cys Lys Arg Phe Asp Gly Ala Asp Ile Tyr Asp Ile
 25 30 35

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tgc atc aag ttc ttc aag gcc aac aag gac agc gcc acc aca gac aag 197
Cys Ile Lys Phe Phe Lys Ala Asn Lys Asp Ser Ala Thr Thr Asp Lys
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cgt ggc ctt gct gtc att gcc act aag att gcc agt gcg aca gct gtg      245
Arg Gly Leu Ala Val Ile Ala Thr Lys Ile Ala Ser Ala Thr Ala Val
          60          65          70
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gac acc cgc aag cgc att gcc atc ctg aag gcc gag gaa aag gac cat . . . 293
 Asp Thr Arg Lys Arg Ile Ala Ile Leu Lys Ala Glu Glu Lys Asp His
 75 80 85

atg atc caa cag gtc ctc gcc tac tgt gac aat atg tac tcc aga gct	341
Met Ile Gln Gln Val Leu Ala Tyr Cys Asp Asn Met Tyr Ser Arg Ala	
90 95 100	
atg ggc ttg ttt gac aaa gct gcc agg ggc atc ttg tca ggc agg ttg	389
Met Gly Leu Phe Asp Lys Ala Ala Arg Gly Ile Leu Ser Gly Arg Leu	
105 110 115	
ggc gac gcg gtg acg agc ctc agc tcc gcg ttg gat att ccc aaa tat	437
Gly Asp Ala Val Thr Ser Leu Ser Ala Leu Asp Ile Pro Lys Tyr	
120 125 130 135	
tgc gat gac gag ttc ctc gag gca ggc gtg aag tca ccg ttc gat gcc	485
Cys Asp Asp Glu Phe Leu Glu Ala Gly Val Lys Ser Pro Phe Asp Ala	
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gag aac agc gag ttc gag atg caa tgt gcc ata act ctg ggt gta acg	533
Glu Asn Ser Glu Phe Glu Met Gln Cys Ala Ile Thr Leu Gly Val Thr	
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Lys Met Leu Thr Phe *	
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Gly Ala Asp Ile Tyr Asp Ile Cys Ile Lys Phe Phe Lys Ala Asn Lys	
35 40 45	
Asp Ser Ala Thr Thr Asp Lys Arg Gly Leu Ala Val Ile Ala Thr Lys	
50 55 60	
Ile Ala Ser Ala Thr Ala Val Asp Thr Arg Lys Arg Ile Ala Ile Leu	
65 70 75 80	
Lys Ala Glu Glu Lys Asp His Met Ile Gln Gln Val Leu Ala Tyr Cys	
85 90 95	
Asp Asn Met Tyr Ser Arg Ala Met Gly Leu Phe Asp Lys Ala Ala Arg	
100 105 110	
Gly Ile Leu Ser Gly Arg Leu Gly Asp Ala Val Thr Ser Leu Ser Ser	
115 120 125	
Ala Leu Asp Ile Pro Lys Tyr Cys Asp Asp Glu Phe Leu Glu Ala Gly	
130 135 140	
Val Lys Ser Pro Phe Asp Ala Glu Asn Ser Glu Phe Glu Met Gln Cys	
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Ser Leu Leu Val Val Val Leu Leu Leu Ala Ser Ser Ser Ala Ser Val
10 15 20

ata gaa gac aca tgc agg cgc ttc gat ggt gct gac atc tac gat atc 149
Ile Glu Asp Thr Cys Arg Arg Phe Asp Gly Ala Asp Ile Tyr Asp Ile
25 30 35

tgc atc aag ttc ttc aag gcc aac aag gat agc gcc acc acg gac aag 197
Cys Ile Lys Phe Phe Lys Ala Asn Lys Asp Ser Ala Thr Thr Asp Lys
40 45 50 55

cgt ggc ctt gct gtc atc gcc att ggg att gcc agt gcg aca gct gtg 245
Arg Gly Leu Ala Val Ile Ala Ile Gly Ile Ala Ser Ala Thr Ala Val
60 65 70

gac acc cgc aag cgc gtc gcc acc ctg aag gcc gag gaa aag gat caa 293
Asp Thr Arg Lys Arg Val Ala Thr Leu Lys Ala Glu Glu Lys Asp Gln
75 80 85

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gtg ggc cta ttt gac aag gct gcc agg ggc atc tcg ttg ggc agg ttg Val Gly Leu Phe Asp Lys Ala Ala Arg Gly Ile Ser Leu Gly Arg Leu 105 110 115	389
ggc gac gca gtg acg agc ctc agc tcc gca ctg gac att ccc aaa tat Gly Asp Ala Val Thr Ser Leu Ser Ala Leu Asp Ile Pro Lys Tyr 120 125 130 135	437
tgc gat gac aag ttc ctc gag gca ggc gtg aag tcg cca ttc gat gcc Cys Asp Asp Lys Phe Leu Glu Ala Gly Val Lys Ser Pro Phe Asp Ala 140 145 150	485
gag aac agc gag ttc gag gtg caa tgt gca atc act ctg ggt gta acg Glu Asn Ser Glu Phe Glu Val Gln Cys Ala Ile Thr Leu Gly Val Thr 155 160 165	533
aag atg ctg acc atg tag ttagcgagtc ggcgaggaca tgaatgtggg Lys Met Leu Thr Met *	581
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Ile Ala Ser Ala Thr Ala Val Asp Thr Arg Lys Arg Val Ala Thr Leu 65 70 75 80	
Lys Ala Glu Glu Lys Asp Gln Ile Ile Gln His Val Leu Ala Tyr Cys 85 90 95	
Asp Asn Met Tyr Ser Ser Val Val Gly Leu Phe Asp Lys Ala Ala Arg 100 105 110	
Gly Ile Ser Leu Gly Arg Leu Gly Asp Ala Val Thr Ser Leu Ser Ser 115 120 125	
Ala Leu Asp Ile Pro Lys Tyr Cys Asp Asp Lys Phe Leu Glu Ala Gly 130 135 140	
Val Lys Ser Pro Phe Asp Ala Glu Asn Ser Glu Phe Glu Val Gln Cys 145 150 155 160	

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aaggccgagg	aaaaggatca	aattatccag	catgtcctcg	cctactgtga	caatatgtac	300
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gacgcagtga	cgagcctcag	ctccgcactg	gacattccca	aatattgcga	tgacaagttc	420
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